WHAT IS CLAIMED IS:

1. A method of typing a growth arising in association with a congenital melanocytic nevus, the method comprising providing a skin tumor sample from a patient and detecting a change in chromosome number in a nucleic acid sample from the skin tumor sample, wherein the change in chromosome number is selected from the group consisting of a gain of chromosome 10, a gain of chromosome 11, a loss of chromosome 7, or a combination thereof; thereby typing the skin tumor sample as a benign growth.

2. The method of claim 1, wherein the change in chromosome number is a gain of chromosome 10.

3. The method of claim 1, wherein the change in chromosome number is a gain of chromosome 11.

4. The method of claim 1, wherein the change in chromosome number is a loss of chromosome 7.

5. The method of claim 1, further comprising detecting a gain or loss of another chromosome.

6. The method of claim 1, wherein the detecting step comprises:

contacting a nucleic acid sample from the patient with a probe which selectively hybridizes to a target polynucleotide sequence on a chromosome selected from the group consisting of chromosome 10, chromosome 11, and chromosome 7; wherein the probe is contacted with the sample under conditions in which the probe binds selectively with the target polynucleotide sequence to form a stable hybridization complex;

detecting the formation of the hybridization complex; and

detecting a change in chromosome number, the change selected from the group consisting of a gain of chromosome 10, a gain of chromosome 11 and a loss of chromosome 7.

7. The method of claim 6, wherein the detecting step further comprises amplifying the target nucleotide sequence.

8. The method of claim 7, wherein the target nucleotide sequence is amplified using a polymerase chain reaction.

9. The method of claim 6, wherein the eprobe is a centromeric probe.

10. The method of claim 1, wherein the nucleic acid sample is an interphase nucleus.

11. The method of claim 1, wherein the nucleic acid sample is a metaphase cell.

12. The method of claim 6, wherein the probe is labeled with a fluorescent label.

13. The method of claim 6, wherein the probe is labeled with digoxigenin or biotin.

14. The method of claim 6, further comprising the step of blocking the hybridization capacity of repetitive sequences in the nucleic acid sample.

15. The method of claim 14, wherein unlabeled blocking nucleic acids comprising repetitive sequences are contacted with the sample.

16. The method of claim 15, wherein the unlabeled blocking nucleic acids are Cot-1 DNA.

17. The method of claim 6, wherein the probe is bound to a solid substrate.

18. The method of claim 17, wherein the probe is a member of an array.